[0013] Accordingly, the invention provides a γ-Netrin-binding peptide, comprising (i) the sequence EVMPTLDMALFDWTDYEDLKP (SEQ ID NO.: 1), or (ii) the sequence DVAPTFNMALFDWTDYEDMRP (SEQ ID NO.: 2), or (iii) the sequence EVMPTLDMTLFDWTDYEDMKP (SEQ ID NO.: 3), or (iv) a variant thereof having a sequence identity of at least 70%, at least 80%, at least 85%, at least 90%, or at least 95% to SEQ ID NO.: 1, 2 and/or 3, wherein said peptide has a length of up to 328 amino acids and is optionally fused to a heterologous peptide or polypeptide. Preferably, the γ-Netrin is Netrin1.

[0014] The γ-Netrin-binding peptide is characterized in that it binds with high affinity to Netrins derived from the γ chain of Laminin1, comprising in particular human Netrin1 and human Netrin3 as well as Netrins 1a, 1b and 2 from zebrafish (*Danio rerio*). In particular, the γ-Netrin-binding peptide of the invention binds to human Netrin1 and to zebrafish Netrin1a (also referred to as Ntn1a) and Netrin1b (also referred to as Ntn1b). In preferred embodiments, it is therefore referred to as "Netrin1-binding peptide".

[0015] In some embodiments, the peptide with a length of up to 328 amino acids comprises any one of SEQ ID NO.: 1, 2, 3 or a variant thereof having a sequence identity of at least 70%, at least 80%, at least 85%, at least 90%, or at least 95% to SEQ ID NO.: 1, 2 and/or 3 and is free of any further heterologous peptides.

[0016] In other embodiments, the peptide with a length of up to 328 amino acids comprises any one of SEQ ID NO.: 1, 2, 3 or a variant thereof having a sequence identity of at least 70%, at least 80%, at least 85%, at least 90%, or at least 95% to SEQ ID NO.: 1, 2 and/or 3 and is fused to a heterologous peptide or polypeptide as defined below.

[0017] The minimal sequence of the γ-Netrin-binding peptide, in particular Netrin1-binding peptide is represented by

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                                    SEQ ID NO.: 1
EVMPTLDMALFDWTDYEDLKP,

                                    SEQ ID NO.: 2
DVAPTFNMALFDWTDYEDMRP,
and

                                    SEQ ID NO.: 3
EVMPTLDMTLFDWTDYEDMKP, respectively.
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[0018] In some embodiments, the peptide has a length of up to 328 amino acids, up to 324 amino acids, up to 320 amino acids, up to 250 amino acids, up to 200 amino acids, up to 100 amino acids, up to 50 amino acids, or up to 30 amino acids. According to other embodiments, the peptide has a length of up to 150 amino acids or up to 125 amino acids. Fragments comprising up to 50 amino acids are preferred according to some embodiments.

[0019] In certain preferred embodiments, a variant of SEQ ID NO.: 1, SEQ ID NO.: 2 or SEQ ID NO.: 3 have a sequence identity of at least 70% to SEQ ID NO.: 1, 2 and/or 3. In further embodiments the level of sequence identity may be at least 90%, or even at least 95% to SEQ ID NO.: 1, 2 and/or 3.

[0020] A "variant" in the context of the present invention is any peptide whose amino acid sequence varies in at least one position from the respective reference peptide, but retains the biological activity of the reference peptide; for example, a variant of SEQ ID NO.: 1 differs in at least one amino acid therefrom, and retains the γ-Netrin-, particularly Netrin1-binding activity. In particular, variants of SEQ ID NO.: 1, 2 and 3 differ in 1, 2, 3, 4, 5, 6 or 7 amino acids from SEQ ID NO.: 1, SEQ ID NO.: 2 and/or SEQ ID NO.: 3, provided they retain the γ-Netrin-, particularly Netrin1-binding activity. Variations will usually be generated by amino acid substitutions. Particularly, a variant according to the invention will be characterized in that it has been changed to contain at least one non-naturally occurring substitution modification relative to the respective reference peptide.

[0021] The peptidic compounds of the present invention comprise a linear backbone of amino carboxylic acids linked by peptide, i.e. carboxamide bonds. Preferably, the amino carboxylic acids are α-amino carboxylic acids and more preferably L-α-amino carboxylic acids, unless indicated otherwise. Any amino acid of the sequences disclosed herein may be replaced either by an unmodified canonical proteinogenic L-amino acid, or by an unmodified canonical proteinogenic D-amino acid. Also envisaged are substitutions with non-canonical proteinogenic amino acids, in particular with ornithine, 2,4-diamino butyric acid, 2,3-diamino propionic acid, selenocysteine, pyrrolysine, hydroxyproline, O-phosphoserine, O-phosphotyrosin, γ-carboxyglutamic acid, γ-aminobutyric acid, norleucine, ε-aminohexanoic acid, and with other posttranslationally modified amino acids, e.g. amino acids with amidated carboxyl groups (at C-termini of peptides), amino acids with alkylated (e.g. methylated) side chains, amino acids with an amino side chain group (such as lysine and ornithine) with modifications at one or both of the hydrogen atoms of the amino side chain group, for example with a lipophilic moiety attached via a carboxamide bond, etc.

[0022] The percent sequence identity may be determined according to the following formula:

$$I=n:L$$

wherein I is the identity in percent, n is the number of identical amino acids between a given sequence and a comparative sequence as shown e.g. in SEQ ID NOs.: 1, 2 and 3, and L is the length of the comparative sequence. Importantly, when calculating the percent sequence identity according to this formula, an alignment of the two sequences shall be carried out without gaps between complementary portions and over the whole length of the comparative sequence.

[0023] In specific embodiments, the invention provides a γ-Netrin-binding peptide, comprising (i) the sequence EVMPTLDMALFDWTDYEDLKP (SEQ ID NO.: 1), or (ii) the sequence DVAPTFNMALFDWTDYEDMRP (SEQ ID NO.: 2), or (iii) the sequence EVMPTLDMTLFDWTDYEDMKP (SEQ ID NO.: 3), or (iv) a variant thereof having a sequence identity of at least 70%, at least 80%, at least 85%, at least 90%, or at least 95% to SEQ ID NO.: 1, 2 and/or 3, wherein said peptide has a length of up to 100 amino acids and is optionally fused to a heterologous peptide or polypeptide.

[0024] According to some embodiments, the γ-Netrin-binding peptide, in particular the Netrin1-binding peptide, comprises any one of SEQ ID NO.: 7, SEQ ID NO.: 8, SEQ ID NO.: 9, SEQ ID NO.: 10, SEQ ID NO.: 11, SEQ ID NO.: 12, SEQ ID NO.: 13, SEQ ID NO.: 14 or SEQ ID NO.: 15 or a corresponding fragment of another species. Preferably, the peptide comprises any one of SEQ ID NO.: 10, SEQ ID NO.: 11, SEQ ID NO.: 12, SEQ ID NO.: 13, SEQ ID NO.: